



National  
Library  
of Medicine



Entrez PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Book

Search  for

Limits

Preview/Index

History

Clipboard

Details

About Entrez

Show:  Sort

Text Version

1: J Biotechnol. 1999 Feb 19;68(2-3):101-13.

Related Articles, L

Entrez PubMed

Overview

Help | FAQ

Tutorial

New/Noteworthy

E-Utilities

PubMed Services

Journals Database

MeSH Database

Single Citation Matcher

Batch Citation Matcher

Clinical Queries

LinkOut

Cubby

Related Resources

Order Documents

NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

Privacy Policy

## Cloning, nucleotide sequence and expression of a new L-N-carbamoylase gene from *Arthrobacter aurescens* DSM 3747 in *E. coli*.

Wilms B, Wiese A, Syldatk C, Mattes R, Altenbuchner J, Pietzsch M.

Institute of Industrial Genetics, University of Stuttgart, Germany.

An L-N-carbamoyl amino acid amidohydrolase (L-N-carbamoylase) from *Arthrobacter aurescens* DSM 3747 was cloned in *E. coli* and the nucleotide sequence was determined. After expression of the gene in *E. coli* the enzyme was purified to homogeneity and characterized. The enzyme was shown to be strictly L-specific and exhibited the highest activity in the hydrolysis of beta-aryl substituted N alpha-carbamoyl-alanines as e.g. N-carbamoyl-tryptophan. Carbamoyl derivatives of beta-alanine and charged aliphatic amino acids were not accepted as substrates. The N-carbamoylase of *A. aurescens* DSM 3747 differs from all known enzymes with respect to its substrate specificity although amino acid sequence identity scores of 35-38% to other N-carbamoylases have been detected. The enzyme consists of two subunits of 44,000 Da, and has an isoelectric point of 4.3. The optima of temperature and pH were determined to be 50 degrees C and pH 8.5 respectively. At 37 degrees C the enzyme was completely stable for several days.

PMID: 10194852 [PubMed - indexed for MEDLINE]

Show:  Sort

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Freedom of Information Act](#) | [Disclaimer](#)

Apr 19 2004 06:



National  
Library  
of Medicine

Entrez PubMed

Nucleotide

Protein

Genome

Structure

OMIM

PMC

Journals

Book

Search  for

Limits

Preview/Index

History

Clipboard

Details

About Entrez

Show:  Sort

Text Version

1: FEMS Microbiol Lett. 1996 Nov 15;145(1):55-62.

Related Articles, L

FULL-TEXT ARTICLE

## Identification, sequencing and mutagenesis of the gene for a D-carbamoylase from *Agrobacterium radiobacter*.

**Buson A, Negro A, Grassato L, Tagliaro M, Basaglia M, Grandi C, Fontana A, Nut MP.**

CRIBI Biotechnology Centre, University of Padua, Italy. albe@civ.bio.unipd.it

A clone positive for D-carbamoylase activity (2.7 kb HindIII-BamHI DNA fragment) was obtained by screening a genomic library of *Agrobacterium radiobacter* in *Escherichia coli*. This DNA fragment contains an open reading frame of 912 bp which is predicted to encode a peptide of 304 amino acids with a calculated molecular mass of 34247 Da. The D-carbamoylase gene, named cauA, was placed under the control of T7 RNA-dependent promoter and expressed in *E. coli* BL21(DE3). After induction with isopropyl-thio-beta-galactopyranoside, the synthesis of D-carbamoylase in *E. coli* reached about 40% of the total protein. The expressed protein was shown to possess a molecular mass, on SDS-PAGE, of 36 kDa and showed an enhanced stability with respect to that of the wild-type enzyme derived from *A. radiobacter*. Site-directed mutagenesis experiments allowed us to establish that a Pro14-->Leu14 exchange leads to an inactive enzyme species, while a Cys279-->Ser279 exchange did not impair the functional properties of the enzyme.

PMID: 8931327 [PubMed - indexed for MEDLINE]

Show:  Sort

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Freedom of Information Act](#) | [Disclaimer](#)